

NATURE 2001

83% identity to SEQ ID NO:1 but not annotated as sphingomyelinase

<!--StartFragment-->NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta, and Intestinal mucosa;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta, and Intestinal mucosa;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [7]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta, and Intestinal mucosa;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y.;

RT "RIKEN integrated sequence analysis (RISA) system--384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [8]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

RN [9]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Intestinal mucosa;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AK144474; BAE25908.1; -; mRNA.
DR EMBL; AK167678; BAE39727.1; -; mRNA.
DR UniGene; Mm.244114; -.
DR Ensembl; ENSMUSG00000046697; Mus musculus.
DR MGI; MGI:3027917; Enpp7.
DR GO; GO:0008152; P:metabolic process; IEA:InterPro.
DR InterPro; IPR001952; Alk_phosphatase. it is not annotated as sphingomyelinase
DR InterPro; IPR002591; Phosphodiesterase.
DR Gene3D; G3DSA:3.40.720.10; Alk_phosphatase; 1.
DR Pfam; PF01663; Phosphodiesterase; 1.
PE 2: Evidence at transcript level;
SQ SEQUENCE 439 AA; 49618 MW; 5D6112A945136709 CRC64;

Query Match 75.6%; Score 1868.5; DB 2; Length 439;
Best Local Similarity 82.9%; Pred. No. 2e-137;
Matches 343; Conservative 34; Mismatches 34; Indels 3; Gaps 1;

Qy	5	AVLLTVALATLLAPGAGAPVQSQGSQNKLLLVSFDFGRWNYDQDVDTPNLDAMARDGVKA	64
		:	
Db	5	AVLLCVALAILPACVTGAPVQ---RQHKLLLVSFDFGRWNYDQDVDTPNLDSMAQEGVKA	61
Qy	65	RYMTPAFVTMTSPCHFTLVTKYIENHGVVHNMYNTTISKVKLPYHATLGIQRWWDNGSV	124
		:	
Db	62	QYMTPAFVTMTSPCHFTLVTKYIENHGVVHNMFYNTTSTVRLPYHATLGIQRWWDNGSI	121
Qy	125	PIWITAQRQGLRAGSFFYPGGNVTYQGVAVTRSRKEGIAHNYKNETEWRANIDTVMMAWFT	184
Db	122	PIWITAQRQGLKTGSFFYPGGNVTYQGEAVTMSRKEGVVHNYKNETEWRGNVDVTVMKWFL	181
Qy	185	EEDLDLVTLTYFGEPDSTGHRYGPESPERREMVRQVDRTVGYLRRESIARNHLTDRLNLIIT	244
		:	
Db	182	EEDVSLVTLYFGEPDSTGHRYGPESQERKDMVKQVDRTVGYLRDSIKRHHLSDSLNLIIIT	241
Qy	245	SDHGTTTVDKRAGDLVEFHKFPNFTFRDIEFELLDYGPNGMLLPKEGRLEKVYDALKDAH	304
Db	242	SDHGTTTVNKKASDLVEFHKFSNFTFQDIQFELLDYGPNGMLLPKEGMLEKVYSVLKDAH	301
Qy	305	PKLHVYKKEAFPEAFHYANNPRVTPLLMYSDLGVIHGRINVQFNNGEHGFDNKDMDMKT	364
		:	
Db	302	PRLHVYKKEDFPKNFHYANNPRITPLLMYSDLGVIHGRVNVQFNNGEHGFNNQDMDMKT	361
Qy	365	IFRAVGPSFRAGLEVPEFESVHVYELMCRLLGIVPEANDGHLATLLPMLHTESA	418
Db	362	IFRAVGPSFKAGLEVPEFESVHVYELMCQLLGIVPEPNDGNPGILRPMLRSGSA	415

RESULT 5
<!--EndFragment-->